What is claimed:

1. An isolated, purified, or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of SEQ ID No 1 or the complements thereof, wherein said contiguous span comprises at least 1 of the following nucleotide positions of SEQ ID No 1: 1-485, 547-632, 827-7291, 7385-13759, 13831-14062, 14671-15054, and 15252-17131.

2. An isolated, purified, or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of SEQ ID No 2 or the complements thereof, wherein said contiguous span comprises at least 1 of the nucleotide positions 834-1217 of SEQ ID No 2.

3. An isolated, purified, or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of SEQ ID No 3 or the complements thereof, wherein said contiguous span comprises at least 1 of the nucleotide positions 967-1351 of SEQ ID No 2.

4. An isolated, purified, or recombinant polynucleotide consisting essentially of a contiguous span of 8 to 50 nucleotides of anyone of SEQ ID Nos 1-3 or the complement thereof, wherein said span includes a *hGGPPS*-related biallelic marker in said sequence.

5. A polynucleotide according to claim 4, wherein said *hGGPPS*-related biallelic marker is the biallelic marker 5-187-77.

6. A polynucleotide according to any one of claims 4 or 5, wherein said contiguous span is 18 to 50 nucleotides in length and said biallelic marker is within 4 nucleotides of the center of said polynucleotide.

7. A polynucleotide according to claim 6, wherein said polynucleotide consists of said contiguous span and said contiguous span is 25 nucleotides in length and said biallelic marker is at the center of said polynucleotide.

8. A polynucleotide according to claim 6, wherein said polynucleotide consists essentially of a sequence selected from the group consisting of SEQ ID Nos 5 and 6 and the complementary sequences thereto.

9. A polynucleotide according to any one of claims 1-5, wherein the 3' end of said contiguous span is present at the 3' end of said polynucleotide.

Sub A3

10. An isolated, purified, or recombinant polynucleotide consisting essentially of a sequence selected from the group consisting of SEQ ID Nos 8-9.

11. A polynucleotide according to any one of claims 4 or 5, wherein the 3' end of said contiguous span is located at the 3' end of said polynucleotide and said biallelic marker is present at the 3' end of said polynucleotide.

12. An isolated, purified, or recombinant polynucleotide consisting essentially of a contiguous span of 8 to 50 nucleotides of anyone of SEQ ID Nos 1-3 or the complement thereof, wherein the 3' end of said contiguous span is located at the 3' end of said polynucleotide, and wherein the 3' end of said polynucleotide is located within 20 nucleotides upstream of a *hGGPPS*-related biallelic marker in said sequence.

13. A polynucleotide according to claim 12, wherein the 3' end of said polynucleotide is located 1 nucleotide upstream of said *hGGPPS* related biallelic marker in said sequence.

14. A polynucleotide according to claim 13, wherein said polynucleotide consists essentially of the sequence of SEQ ID No 7.

Sub A4

15. An isolated, purified, or recombinant polynucleotide which encodes a polypeptide comprising a contiguous span of at least 6 amino acids of SEQ ID No 4, wherein said contiguous span includes at least one amino acid selected from the group consisting of a Phe residue at positions 204, 257, 295 of SEQ ID No 4, a Cys residue at position 205 of SEQ ID No 4, a Pro residue at position 225 of SEQ ID No 4, and a Glu residue at position 252 of SEQ ID No 4.

16. A polynucleotide for use in a genotyping assay for determining the identity of the nucleotide at a *hGGPPS*-related biallelic marker or the complement thereof.

17. A polynucleotide according to claim 16, wherein the polynucleotide is used in a hybridization assay.

18. A polynucleotide according to claim 16, wherein the polynucleotide is used in a sequencing assay.

19. A polynucleotide according to claim 16, wherein the polynucleotide is used in an enzyme-based mismatch detection assay.

20. A polynucleotide according to claim 16, wherein the polynucleotide is used in amplifying a segment of nucleotides comprising said biallelic marker.

Sub A5

21. A polynucleotide according to any one of claims 1-20 attached to a solid support.

22. An array of polynucleotides comprising at least one polynucleotide according to claim 21.

23. An array according to claim 22, wherein said array is addressable.

Sub A6

24. A polynucleotide according to any one of claims 1-20 further comprising a label.

25. A recombinant vector comprising a polynucleotide according to any one of claims 1-20.

26. A host cell comprising a recombinant vector according to claim 25.

27. A non-human host animal or mammal comprising a recombinant vector according to claim 25.

28. A method of genotyping comprising determining the identity of a nucleotide at a *hGGPPS*-related biallelic marker or the complement thereof in a biological sample.

29. A method according to claim 28, wherein said biological sample is derived from a single subject.

30. A method according to claim 29, wherein the identity of the nucleotides at said biallelic marker is determined for both copies of said biallelic marker present in said individual's genome.

31. A method according to claim 28, wherein said biological sample is derived from multiple subjects.

Sub A7

32. A method according to any one of claims 28, further comprising amplifying a portion of said sequence comprising the biallelic marker prior to said determining step.

33. A method according to claim 32, wherein said amplifying is performed by PCR.

34. A method according to any one of claims 28-33, wherein said determining is performed by a hybridization assay.

35. A method according to any one of claims 28-33, wherein said determining is performed by a sequencing assay.

36. A method according to any one of claims 28-33, wherein said determining is performed by a microsequencing assay.

37. A method according to any one of claims 28-33, wherein said determining is performed by an enzyme-based mismatch detection assay.

38. An isolated, purified, or recombinant polypeptide comprising a contiguous span of at least 6 amino acids of SEQ ID No 4, wherein said contiguous span includes at least one amino acid selected from the group consisting of a Phe residue at positions 204, 257, 295 of SEQ ID No 4, a Cys residue at position 205 of SEQ ID No 4, a Pro residue at position 225 of SEQ ID No 4, and a Glu residue at position 252 of SEQ ID No 4.

39. An isolated or purified antibody composition are capable of selectively binding to an epitope-containing fragment of a polypeptide according to claim 38, wherein said epitope comprises at least one amino acid selected from the group consisting of a Phe residue at positions 204, 257, 295 of SEQ ID No 4, a Cys residue at position 205 of SEQ ID No 4, a Pro residue at position 225 of SEQ ID No 4, and a Glu residue at position 252 of SEQ ID No 4.

40. A method for the screening of a candidate substance or molecule modulating the expression of the *hGGPS* gene, said method comprising the following steps :

a) providing a recombinant host cell expressing a nucleic acid, wherein said nucleic acid comprises a nucleotide sequence selected from the group consisting of SEQ ID Nos 1, 2 and 3 or a fragment thereof;

b) obtaining a candidate substance, and

c) determining the ability of the candidate substance to modulate the expression levels of the nucleotide sequence selected from the group consisting of SEQ ID Nos 1, 2 and 3 or a fragment thereof.

41. A method for the screening of a candidate substance or molecule modulating the expression of the *hGGPS* gene, said method comprising the following steps :

- providing a recombinant cell host containing a nucleic acid, wherein said nucleic acid comprises a nucleotide sequence of the 5' regulatory region or a biologically active fragment or variant thereof located upstream a polynucleotide encoding a detectable protein;
- obtaining a candidate substance; and
- determining the ability of the candidate substance to modulate the expression levels of the polynucleotide encoding the detectable protein.